



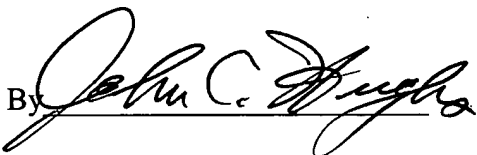
**REMARKS/ARGUMENTS**

In accordance with the Objection to the Sequence Listing, the Specification has been amended to comply and remove all objections and errors. A computer readable form copy of the Sequence Listing has been included with this mailing. Please note that the substitute paper copy of the sequence listing and the computer readable form copy are identical and do not contain any new matter.

Applicant respectfully requests that the patent issue as soon as possible.

Respectfully submitted,

NORTHWEST PATENT LAW

By 

John C. Hughs

Reg. No. 47,236

Tel.: (509) 332-4995





SEQUENCE LISTING-revised 2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Joseph W Harding and John W Wright
- (ii) TITLE OF INVENTION: AT4 Ligands as Anti-Angiogenic and Anti-Tumor Agents
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Pacific Northwest Biotechnology, Inc.
  - (B) STREET: SE 745 Derby Street
  - (C) CITY: Pullman
  - (D) STATE: Washington
  - (E) COUNTRY: United States of America
  - (F) ZIP: 99163
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: CD, 700MB
  - (B) COMPUTER: PC
  - (C) OPERATING SYSTEM: WINDOWS XP
  - (D) SOFTWARE: OFFICE WORD
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 10/675,470
  - (B) FILING DATE: 09/30/2003
  - (C) CLASSIFICATION: 530/300
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: John Hughes
  - (B) REGISTRATION NUMBER: 47,236
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (509) 335-7927; (509) 332-3178
  - (B) TELEFAX: (509) 335-4650

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Xaa is norleucine
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
Xaa Tyr Ile His

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Xaa(1) is norleucine; Xaa(4) is 6-aminohexanoic acid; amidation
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
Xaa Tyr Ile Xaa

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (ix) FEATURE:

SEQUENCE LISTING-revised 2

- (D) OTHER INFORMATION: Xaa(1) is Norleucine  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
Xaa Tyr Ile His Pro Phe  
5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: N-terminal  
(ix) FEATURE:

bond (D) OTHER INFORMATION: Xaa is norleucine; Leu(3)-His(4) has a methylene

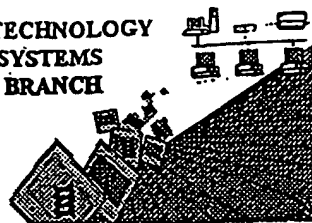
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
Xaa Tyr Leu His Pro Phe  
5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: N-terminal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
Val Tyr Ile His Pro Phe  
5



BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/675,470

Source:

1-1-016

Date Processed by STIC:

7-4-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,  
Room 1B03, Arlington, VA 22202

Revised 05/17/04

58



IFW16

## RAW SEQUENCE LISTING

DATE: 01/04/2005

PATENT APPLICATION: US/10/675,470

TIME: 10:02:47

Input Set : A:\SEQUENCE LISTING.asc

Output Set: N:\CRF4\01042005\J675470.raw

## SEQUENCE LISTING

2 (1) GENERAL INFORMATION:  
 3 (iii) NUMBER OF SEQUENCES: 4  
 C--> 0 (vi) CURRENT APPLICATION DATA:  
 C--> 0 (A) APPLICATION NUMBER: US/10/675,470  
 C--> 0 (B) FILING DATE: 30-Sep-2003

## ERRORED SEQUENCES

5 (2) INFORMATION FOR SEQ ID NO: 1:  
 6 (i) SEQUENCE CHARACTERISTICS:  
 7 (A) LENGTH: 4 amino acids  
 8 (B) TYPE: amino acid  
 9 (C) STRANDEDNESS: single  
 10 (D) TOPOLOGY: linear  
 11 (ii) MOLECULE TYPE: peptide  
 12 (iii) HYPOTHETICAL: NO  
 13 (iv) ANTI-SENSE: NO  
 14 (v) FRAGMENT TYPE: N-terminal  
 15 (vi) ORIGINAL SOURCE:  
 16 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 E--> 17 ~~Norleucine Tyr Cys His~~  
 19 (2) INFORMATION FOR SEQ ID NO: 2:  
 20 (i) SEQUENCE CHARACTERISTICS:  
 21 (A) LENGTH: 4 amino acids  
 22 (B) TYPE: amino acid  
 23 (C) STRANDEDNESS: single  
 24 (D) TOPOLOGY: linear  
 25 (ii) MOLECULE TYPE: peptide  
 26 (iii) HYPOTHETICAL: NO  
 27 (iv) ANTI-SENSE: NO  
 28 (v) FRAGMENT TYPE: N-terminal  
 29 (vi) ORIGINAL SOURCE:  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 E--> 31 ~~Norleucine Tyr Cys (6-Aminohexanoic Acid) -amide~~  
 34 (2) INFORMATION FOR SEQ ID NO: 3:  
 35 (i) SEQUENCE CHARACTERISTICS:  
 36 (A) LENGTH: 6 amino acids  
 37 (B) TYPE: amino acid  
 38 (C) STRANDEDNESS: single  
 39 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: peptide

Does Not Comply  
 Corrected Diskette Needed

Amino Acid (pg. 1-2) ←

pls use (3) letter  
 base codes.

delete

pls use (3) letter  
 Amino acid base codes.

delete

↑ FYI: PLS use sequencing format  
 per OLD rule 5/14/05



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/675,470

DATE: 01/04/2005  
TIME: 10:02:47

Input Set : A:\SEQUENCE LISTING.asc  
Output Set: N:\CRF4\01042005\J675470.raw

41 (A) DESCRIPTION: Norleucine(1)- Angiotensin IV  
42 (iii) HYPOTHETICAL: NO  
43 (iv) ANTI-SENSE: NO  
44 (v) FRAGMENT TYPE: N-terminal  
C--> 45 (vi) ORIGINAL SOURCE:  
46 (ix) FEATURE:  
47 (A) NAME/KEY: Modified-site  
48 (B) LOCATION: N-terminal amino acid  
49 (D) OTHER INFORMATION:  
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
E--> 51 ~~Norleucine-Tyr-Ile-His-Pro-Phe~~  
54 (2) INFORMATION FOR SEQ ID NO: 4:  
55 (i) SEQUENCE CHARACTERISTICS:  
56 (A) LENGTH: 6 amino acids  
57 (B) TYPE: amino acid  
58 (C) STRANDEDNESS: single  
59 (D) TOPOLOGY: linear  
60 (ii) MOLECULE TYPE: peptide  
61 (A) DESCRIPTION: Norleual  
62 (iii) HYPOTHETICAL: NO  
63 (iv) ANTI-SENSE: NO  
64 (v) FRAGMENT TYPE: N-terminal  
65 (vi) ORIGINAL SOURCE:  
66 (ix) FEATURE:  
67 (A) NAME/KEY: Modified-site  
68 (B) LOCATION: Multiple  
69 (D) OTHER INFORMATION:  
70 /note= Leu3-His4 is a methylene bond  
71 instead of a peptide bond.  
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
E--> 73 ~~Norleucine-Tyr-Leu-His-Pro-Phe~~

pls use (3) letter base codes.

pls refer to 1.822 old Sequence Rules Format

pls use (3) letter base codes.

Same error

↑ FYI: Amino acid sequence should be grouped as:

Tyr Leu His Pro

↑ pls use (3) letter

BUT

## VERIFICATION SUMMARY

DATE: 01/04/2005

PATENT APPLICATION: US/10/675,470

TIME: 10:02:48

Input Set : A:\SEQUENCE LISTING.asc

Output Set: N:\CRF4\01042005\J675470.raw

L:0 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1)  
 L:0 M:200 E: Mandatory Header Field missing, [(ii) TITLE OF INVENTION:] of (1)  
 L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)  
 L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)  
 L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]  
 L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]  
 L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]  
 L:17 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:17 M:330 E: (2) Invalid Amino Acid Designator, 1  
 L:17 M:203 E: No. of Seq. differs, LENGTH:Input:4 Found:1 SEQ:1  
 L:31 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:31 M:330 E: (2) Invalid Amino Acid Designator, 2  
 L:31 M:203 E: No. of Seq. differs, LENGTH:Input:4 Found:2 SEQ:2  
 L:45 M:220 C: Keyword misspelled or invalid format, [(vi) ORIGINAL SOURCE:]  
 L:51 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:51 M:330 E: (2) Invalid Amino Acid Designator, 1  
 L:51 M:203 E: No. of Seq. differs, LENGTH:Input:6 Found:1 SEQ:3  
 L:73 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:73 M:330 E: (2) Invalid Amino Acid Designator, 1  
 L:73 M:203 E: No. of Seq. differs, LENGTH:Input:6 Found:1 SEQ:4

B.F.